

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/462,355DATE: 08/18/95  
TIME: 16:03:25

INPUT SET: S5634.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

## (1) General Information:

(i) APPLICANT: Coleman, Roger  
Au-Young, Janice  
Bandman, Olga  
Seilhamer, Jeffrey J.

ENTERED

(ii) TITLE OF INVENTION: C5a-Like Seven Transmembrane Receptor

(iii) NUMBER OF SEQUENCES: 2

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
(B) STREET: 3330 Hillview Avenue  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 94304

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Luther, Barbara J.  
(B) REGISTRATION NUMBER: 33954  
(C) REFERENCE/DOCKET NUMBER: PF-0040 US

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415-855-0555  
(B) TELEFAX: 415-852-0195

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1446 base pairs

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/462,355DATE: 08/18/95  
TIME: 16:03:28

INPUT SET: S5634.raw

47 (B) TYPE: nucleic acid  
48 (C) STRANDEDNESS: single  
49 (D) TOPOLOGY: linear  
50

51 (ii) MOLECULE TYPE: cDNA  
52  
53

54 (vii) IMMEDIATE SOURCE:  
55 (A) LIBRARY: Mast Cell  
56 (B) CLONE: 8118  
57  
58  
59

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
61

62	ATGGCGTCTT TCTCTGCTGA GACCAATTCA ACTGACCTAC TCTCACAGCC ATGGAATGAG	60
63		
64	CCCCCAGTAA TTCTCTCCAT GGTCATTCTC AGCCTTACTT TTTTACTGGG ATTGCCAGGC	120
65		
66	AATGGGCTGG TGCTGTGGGT GGCTGGCCTG AAGATGCAGC GGACAGTGAA CACAATTTGG	180
67		
68	TTCTTCCACC TCACCTTGGC GGACCTCCTC TGCTGCCTCT CCTTGGCCTT CTCGCTGGCT	240
69		
70	CACTTGGCTC TCCAGGGACA GTGGCCCTAC GGCAGGTTCC TATGCAAGCT CATCCCCCTC	300
71		
72	ATCATTGTCC TCAACATGTT TGGCAGTGTC TTCCTGCTTA CTGCCATTAG CCTGGATCGC	360
73		
74	TGTCTTGTGG TATTCAAGCC AATCTGGTGT CAGAATCATC GCAATGTAGG GATGGCCTGC	420
75		
76	TCTATCTGTG GATGTATCTG GGTGGTGGCT TTTGTGTTGT GCATTCCTGT GTTCGTGTAC	480
77		
78	CGGGAAATCT TCACTACAGA CAACCATAAT AGATGTGGCT ACAAATTTGG TCTCTCCAGC	540
79		
80	TCATTAGATT ATCCAGACTT TTATGGGGAT CCACTAGAAA ACAGGTCTCT TGAAAACATT	600
81		
82	GTTTCAGCCGC CTGGAGAAAT GAATGATAGG TTAGATCCTT CCTCTTTCCA AACAAATGAT	660
83		
84	CATCCTTGGA CAGTCCCCAC TGTCTTCCAA CCTCAAACAT TTCAAAGACC TTCTGCAGAT	720
85		
86	TCACTCCCTA GGGGTTCTGC TAGGTTAACA AGTCAAAATC TGTATTCTAA TGTATTTAAA	780
87		
88	CCTGCTGATG TGGTCTCACC TAAAATCCCC AGTGGGTTTC CTATTGAAGA TCACGAAACC	840
89		
90	AGCCCACTGG ATAACCTCTGA TGCTTTTCTC TCTACTCATT TAAAGCTGTT CCCTAGCGCT	900
91		
92	TCTAGCAATT CCTTCTACGA GTCTGAGCTA CCACAAGGTT TCCAGGATTA TTACAATTTA	960
93		
94	GGCCAATTCA CAGATGACGA TCAAGTGCCA ACACCCCTCG TGGCAATAAC GATCACTAGG	1020
95		
96	CTAGTGGTGG GTTTCCTGCT GCCCTCTGTT ATCATGATAG CCTGTTACAG CTTCAATTGTC	1080
97		
98	TTCCGAATGC AAAGGGGCCG CTTGCGCAAG TCTCAGAGCA AAACCTTTCG AGTGGCCGTG	1140
99		

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/462,355

DATE: 08/18/95  
TIME: 16:03:32

INPUT SET: S5634.raw

100 GTGGTGGTGG CTGTCTTTCT TGTCTGCTGG ACTCCATACC ACATTTGGGG AGTCCTGTCA 1200  
101  
102 TTGCTTACTG ACCCAGAAAC TCCCTTGGGG AAAACTCTGA TGTCTTGGGA TCATGTATGC 1260  
103  
104 ATTGCTCTAG CATCTGCCAA TAGTTGCTTT AATCCCTTCC TTTATGCCCT CTTGGGGAAA 1320  
105  
106 GATTTTAGGA AGAAAGCAAG GCAGTCCATT CAGGGAATTC TGGAGGCAGC CTTCACTGAG 1380  
107  
108 GAGCTCACAC GTTCCACCCA CTGTCCCTCA AACAATGTCA TTTCAGAAAAG AAATAGTACA 1440  
109  
110 ACTGTG 1446  
111  
112  
113

## (2) INFORMATION FOR SEQ ID NO:2:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: protein

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

125 Met Ala Ser Phe Ser Ala Glu Thr Asn Ser Thr Asp Leu Leu Ser Gln  
126 1 5 10 15  
127  
128 Pro Trp Asn Glu Pro Pro Val Ile Leu Ser Met Val Ile Leu Ser Leu  
129 20 25 30  
130  
131 Thr Phe Leu Leu Gly Leu Pro Gly Asn Gly Leu Val Leu Trp Val Ala  
132 35 40 45  
133  
134 Gly Leu Lys Met Gln Arg Thr Val Asn Thr Ile Trp Phe Leu His Leu  
135 50 55 60  
136  
137 Thr Leu Ala Asp Leu Leu Cys Cys Leu Ser Leu Ala Phe Ser Leu Ala  
138 65 70 75 80  
139  
140 His Leu Ala Leu Gln Gly Gln Trp Pro Tyr Gly Arg Phe Leu Cys Lys  
141 85 90 95  
142  
143 Leu Ile Pro Ser Ile Ile Val Leu Asn Met Phe Gly Ser Val Phe Leu  
144 100 105 110  
145  
146 Leu Thr Ala Ile Ser Leu Asp Arg Cys Leu Val Val Phe Lys Pro Ile  
147 115 120 125  
148  
149 Trp Cys Gln Asn His Arg Asn Val Gly Met Ala Cys Ser Ile Cys Gly  
150 130 135 140  
151  
152 Cys Ile Trp Val Val Ala Phe Val Leu Cys Ile Pro Val Phe Val Tyr

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/462,355

DATE: 08/18/95  
TIME: 16:03:35

INPUT SET: S5634.raw

153	145	150	155	160
154				
155	Arg Glu Ile Phe Thr Thr Asp Asn His Asn Arg Cys Gly Tyr Lys Phe			
156	165	170	175	
157				
158	Gly Leu Ser Ser Ser Leu Asp Tyr Pro Asp Phe Tyr Gly Asp Pro Leu			
159	180	185	190	
160				
161	Glu Asn Arg Ser Leu Glu Asn Ile Val Gln Pro Pro Gly Glu Met Asn			
162	195	200	205	
163				
164	Asp Arg Leu Asp Pro Ser Ser Phe Gln Thr Asn Asp His Pro Trp Thr			
165	210	215	220	
166				
167	Val Pro Thr Val Phe Gln Pro Gln Thr Phe Gln Arg Pro Ser Ala Asp			
168	225	230	235	240
169				
170	Ser Leu Pro Arg Gly Ser Ala Arg Leu Thr Ser Gln Asn Leu Tyr Ser			
171	245	250	255	
172				
173	Asn Val Phe Lys Pro Ala Asp Val Val Ser Pro Lys Ile Pro Ser Gly			
174	260	265	270	
175				
176	Phe Pro Ile Glu Asp His Glu Thr Ser Pro Leu Asp Asn Ser Asp Ala			
177	275	280	285	
178				
179	Phe Leu Ser Thr His Leu Lys Leu Phe Pro Ser Ala Ser Ser Asn Ser			
180	290	295	300	
181				
182	Phe Tyr Glu Ser Glu Leu Pro Gln Gly Phe Gln Asp Tyr Tyr Asn Leu			
183	305	310	315	320
184				
185	Gly Gln Phe Thr Asp Asp Asp Gln Val Pro Thr Pro Leu Val Ala Ile			
186	325	330	335	
187				
188	Thr Ile Thr Arg Leu Val Val Gly Phe Leu Leu Pro Ser Val Ile Met			
189	340	345	350	
190				
191	Ile Ala Cys Tyr Ser Phe Ile Val Phe Arg Met Gln Arg Gly Arg Phe			
192	355	360	365	
193				
194	Ala Lys Ser Gln Ser Lys Thr Phe Arg Val Ala Val Val Val Val Ala			
195	370	375	380	
196				
197	Val Phe Leu Val Cys Trp Thr Pro Tyr His Ile Trp Gly Val Leu Ser			
198	385	390	395	400
199				
200	Leu Leu Thr Asp Pro Glu Thr Pro Leu Gly Lys Thr Leu Met Ser Trp			
201	405	410	415	
202				
203	Asp His Val Cys Ile Ala Leu Ala Ser Ala Asn Ser Cys Phe Asn Pro			
204	420	425	430	
205				

DATE: 08/18/95  
TIME: 16:03:39

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PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/462,355**

DATE: 08/18/95  
TIME: 16:03:40

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Original Text